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4 protein - protein search, using sw model

on on: December 15, 2003, 14:50:12 ; Search time 41 Seconds
(without alignments)

Title: US-09-831-805A-6

Perfect score: 1635

Sequence: 1 MALLRPPRLCARLPLPDFPL.....VNYIRTDEEGDFRKSSFVY 310

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTRIBEL_23:						
1: SP_archaea:*						
2: SP_bacteria:*						
3: SP_fungi:*						
4: SP_human:*						
5: SP_invertebrate:*						
6: SP_mammal:*						
7: SP_mhc:*						
8: SP_organelle:*						
9: SP_Phage:*						
10: SP_plant:*						
11: SP_ratodent:*						
12: SP_virus:*						
13: SP_vertebrate:*						
14: SP_unclassified:*						
15: SP_rvirus:*						
16: SP_bacteriophage:*						
17: SP_archeap:*						
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.						
SUMMARIES						
result No.	Score	Query Match	Length DB	ID	Description	
1	1629	99.6	310	4 Q9BX67	Q9bx67 homo sapien	
2	1629	99.6	355	4 Q8wN18	Q8wN18 homo sapien	
3	1620	99.1	309	4 Q96FL1	Q96fl1 homo sapien	
4	1417	86.7	310	11 Q9DBB7	Q9dbb7 mus musculus	
5	1415	86.5	310	11 Q9ERK4	Q9erk4 mus musculus	
6	1403	85.8	310	11 Q9D1M9	Q9d1m9 mus musculus	
7	481.5	29.4	298	11 Q9UT59	Q9ut59 mus musculus	
8	481.5	29.4	298	11 Q8C5K9	Q8c5k9 mus musculus	
9	478.5	29.3	298	11 Q8CB95	Q8cb95 mus musculus	
10	458.5	28.0	300	11 Q9UYX1	Q9uyx1 rattus norvegicus	
11	449.5	27.5	300	11 Q8VC39	Q8vc39 mus musculus	
12	331	20.2	259	4 Q9Y5B2	Q9y5b2 homo sapien	
13	321	19.6	173	11 Q9UTKD5	Q9utkd5 rattus norvegicus	
14	291	17.8	64	11 Q8BPN59	Q8bpn59 mus musculus	
15	243	15.2	64	11 Q91664	Q91664 xenopus laevis	
16	242.5	14.8	318	11 Q9CWA4	Q9cwa4 mus musculus	
17	242.5	14.8	304	11 Q9CWA4	Q9cwa4 mus musculus	
ALIGNMENTS						
RESULT 1						
ID	Q9BX67	PRELIMINARY;		PRT:	310 AA.	
AC	Q9BX67;	AC				
DT	01-JUN-2001	(TREMBLref.)	17,	Created)		
DT	01-JUN-2001	(TREMBLref.)	17,	Last sequence update)		
DT	01-MAR-2003	(TREMBLref.)	23,	Last annotation update)		
DE	Junctional adhesion molecule 3 precursor (junctional adhesion molecule-3)	(Hypothetical protein FLJ90828).				
DE	JAM-2 OR JAN3					
OS	Homo sapiens (Human)					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
OX	NCTI_TaxID=9606;					
RN	[1]					
RC	Cloning of Human Junctional Adhesion Molecule 3.";					
RA	Cunningham S.A., Arrate M.P., Tran T.M.; Cloning of Human Junctional Adhesion Molecule 3.;					
RT	Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.					
RN	[12]					
RC	SEQUENCE FROM N.A.					
RA	Aurrand-Lions M.A., Johnson-leger C., Wong C., DuPasquier L.; "Heterogeneity of endothelial junctions is reflected by differential expression and specific subcellular localization of the three JAM family members."					
RT						
RL	Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.					
RN	[13]					
RC	SEQUENCE FROM N.A.					
RA	Aurrand-Lions M.A., Johnson-leger C., Lamagna C., Ozaki H., Kita T.; "Junctional adhesion molecules (JAMs) and interendothelial junctions."					
RT						
RL	Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.					
RN	[14]					
RC	SEQUENCE FROM N.A.					
RA	Sachs U.J.H., Eva O., Bergboef H., Santoso S.; "Characterization of Junctional Adhesion Molecule-3 on Human Platelets: A New Member of Immunoglobulin Superfamily."					
RT						

RL Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.

[5] SEQUENCE FROM N.A.

RA Isogai T., Ota T., Nishikawa T., Hayashi K., Otsubki T., Sugiyma T., Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K., Masuno Y., Ono T., Okano K., Yoshihikawa Y., Aotsuka S., Sasaki N., Hattori A., Okumura K., Iwayanagi Project., Ninomiya K.;

RT "NEDO" human cDNA sequencing project.;

RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AJ46101; CAC94776.1; -.

DR EMBL; AJ46101; CAC94776.1; -.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003598; Ig_C2.

DR InterPro; IPR003006; Ig_MHC.

DR Pfam; PF00047; Ig_2.

DR SMART; SM00408; IgG2_1.

DR PROSITE; PS50335; Ig_LIKE; 2.

DR Immunoglobulin domain.

FT CHAIN 76 355 JUNCTION ADHESION MOLECULE 3.

SQ 355 AA; 39602 MW; 8B1577DEA7B1D4F8 CRC64;

RT heart and identification of a candidate gene, JAM3, expressed during cardiogenesis";

RL Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AJ46101; CAC94776.1; -.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003598; Ig_C2.

DR InterPro; IPR003006; Ig_MHC.

DR Pfam; PF00047; Ig_2.

DR SMART; SM00408; IgG2_1.

DR PROSITE; PS50335; Ig_LIKE; 2.

DR Immunoglobulin domain.

FT CHAIN 76 355 JUNCTION ADHESION MOLECULE 3.

SQ 355 AA; 39602 MW; 8B1577DEA7B1D4F8 CRC64;

Query Match 99.6%; Score 1629; DB 4; Length 355;

Best Local Similarity 99.7%; Pred. No. 2.7E-152;

Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match 99.6%; Score 1629; DB 4; Length 310;

Best Local Similarity 99.7%; Pred. No. 2.2E-152;

Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match 99.6%; Score 1629; DB 4; Length 310;

Best Local Similarity 99.7%; Pred. No. 2.2E-152;

Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match 99.6%; Score 1629; DB 4; Length 310;

Best Local Similarity 99.7%; Pred. No. 2.2E-152;

Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match 99.6%; Score 1629; DB 4; Length 310;

Best Local Similarity 99.7%; Pred. No. 2.2E-152;

Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match 99.6%; Score 1629; DB 4; Length 310;

Best Local Similarity 99.7%; Pred. No. 2.2E-152;

Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match 99.6%; Score 1629; DB 4; Length 310;

Best Local Similarity 99.7%; Pred. No. 2.2E-152;

Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match 99.6%; Score 1629; DB 4; Length 310;

Best Local Similarity 99.7%; Pred. No. 2.2E-152;

Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match 99.6%; Score 1629; DB 4; Length 310;

Best Local Similarity 99.7%; Pred. No. 2.2E-152;

Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match 99.6%; Score 1629; DB 4; Length 310;

Best Local Similarity 99.7%; Pred. No. 2.2E-152;

Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Best Local Similarity 99.7%; Pred. No. 2.2E-152;

Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match 99.6%; Score 1629; DB 4; Length 310;

Best Local Similarity 99.7%; Pred. No. 2.2E-152;

Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match 99.6%; Score 1629; DB 4; Length 310;

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Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match 99.6%; Score 1629; DB 4; Length 310;

Best Local Similarity 99.7%; Pred. No. 2.2E-152;

Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match 99.6%; Score 1629; DB 4; Length 310;

Best Local Similarity 99.7%; Pred. No. 2.2E-152;

Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESUME 2

OBWWL8 PRELIMINARY; PRT; 355 AA.

AC 301 DFRHKSSFV1 310

AC 301 DFRHKSSFV1 310

DE Junction adhesion molecule 3.

GN JAM3.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN SEQUENCE FROM N.A.

DE Human T-cell.

DT Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

DR Sequence FROM N.A.

RP Phillips H.M.;

RP Narrowing the critical region within 11q24-qter for hypoplastic left

RT Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.

RL Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AJ46101; CAC94776.1; -.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003598; Ig_C2.

DR InterPro; IPR003006; Ig_MHC.

DR Pfam; PF00047; Ig_2.

DR SMART; SM00408; IgG2_1.

DR PROSITE; PS50335; Ig_LIKE; 2.

DR Immunoglobulin domain.

FT CHAIN 76 355 JUNCTION ADHESION MOLECULE 3.

SQ 355 AA; 39602 MW; 8B1577DEA7B1D4F8 CRC64;

Query Match 99.6%; Score 1629; DB 4; Length 355;

Best Local Similarity 99.7%; Pred. No. 2.7E-152;

Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match 99.6%; Score 1629; DB 4; Length 355;

Best Local Similarity 99.7%; Pred. No. 2.7E-152;

Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match 99.6%; Score 1629; DB 4; Length 355;

Best Local Similarity 99.7%; Pred. No. 2.7E-152;

Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match 99.6%; Score 1629; DB 4; Length 355;

Best Local Similarity 99.7%; Pred. No. 2.7E-152;

Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match 99.6%; Score 1629; DB 4; Length 355;

Best Local Similarity 99.7%; Pred. No. 2.7E-152;

Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match 99.6%; Score 1629; DB 4; Length 355;

Best Local Similarity 99.7%; Pred. No. 2.7E-152;

Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match 99.6%; Score 1629; DB 4; Length 355;

Best Local Similarity 99.7%; Pred. No. 2.7E-152;

Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match 99.6%; Score 1629; DB 4; Length 355;

Best Local Similarity 99.7%; Pred. No. 2.7E-152;

Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match 99.6%; Score 1629; DB 4; Length 355;

Best Local Similarity 99.7%; Pred. No. 2.7E-152;

Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match 99.6%; Score 1629; DB 4; Length 355;

Best Local Similarity 99.7%; Pred. No. 2.7E-152;

Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match 99.6%; Score 1629; DB 4; Length 355;

Best Local Similarity 99.7%; Pred. No. 2.7E-152;

Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match 99.6%; Score 1629; DB 4; Length 355;

Best Local Similarity 99.7%; Pred. No. 2.7E-152;

Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Best Local Similarity 99.7%; Pred. No. 2.7E-152;

Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match 99.6%; Score 1629; DB 4; Length 355;

Best Local Similarity 99.7%; Pred. No. 2.7E-152;

Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match 99.6%; Score 1629; DB 4; Length 355;

Best Local Similarity 99.7%; Pred. No. 2.7E-152;

Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match 99.6%; Score 1629; DB 4; Length 355;

Best Local Similarity 99.7%; Pred. No. 2.7E-152;

Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match 99.6%; Score 1629; DB 4; Length 355;

Best Local Similarity 99.7%; Pred. No. 2.7E-152;

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Query Match 99.6%; Score 1629; DB 4; Length 355;

Best Local Similarity 99.7%; Pred. No. 2.7E-152;

Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match 99.6%; Score 1629; DB 4; Length 355;

Best Local Similarity 99.7%; Pred. No. 2.7E-152;

Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match 99.6%; Score 1629; DB 4; Length 355;

Best Local Similarity 99.7%; Pred. No. 2.7E-152;

Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match 99.6%; Score 1629; DB 4; Length 355;

Best Local Similarity 99.7%; Pred. No. 2.7E-152;

Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match 99.6%; Score 1629; DB 4; Length 355;

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Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Best Local Similarity 99.7%; Pred. No. 2.7E-152;

Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match 99.6%; Score 1629; DB 4; Length 355;

Best Local Similarity 99.7%; Pred. No. 2.7E-152;

Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match 99.6%; Score 1629; DB 4; Length 355;

Best Local Similarity 99.7%; Pred. No. 2.7E-152;

Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match 99.6%; Score 1629; DB 4; Length 355;

Best Local Similarity 99.7%; Pred. No. 2.7E-152;

Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match 99.6%; Score 1629; DB 4; Length 355;

Best Local Similarity 99.7%; Pred. No. 2.7E-152;

Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match 99.6%; Score 1629; DB 4; Length 355;

Best Local Similarity 99.7%; Pred. No. 2.7E-152;

Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match 99.6%; Score 1629; DB 4; Length 355;

Best Local Similarity 99.7%; Pred. No. 2.7E-152;

Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match 99.6%; Score 1629; DB 4; Length 355;

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Best Local Similarity 99.4%; Pred. No. 1.7e-151;	
Matches 307; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	
Qy 2 ALRRPPRILCARLPDFELLFRGCLIGAVNLKSSNRTPVQEFSVELSITIDSQTS 61	DR PROSTIRE; P550835; IG_LIKE; 2.
Db 1 ALRRPPRILCARLPDFELLFRGCLIGAVNLKSSNRTPVQEFSVELSITIDSQTS 60	KW Immunoglobulin domain
Qy 62 DRIEWKIQDDETTYYFDNKIQDGLAIGELGKTSLKINVNTRDSALYRCVARN 121	KW SEQUENCE 310 AA; 34855 MW; C74884EABE234680 CRC64;
Db 61 DRIEWKIQDQTTYYFDNKIQDGLAIGELGKTSLKINVNTRDSALYRCVARN 120	Best Local Similarity 86.1%; Score 1417; DB 11; Length 310; Pred. No. 2e-131;
Qy 122 DRKEIDEVIEELTVKPKVTPICRUPKAQVPGMATHQCESEGHRRPHYSWYRNIDLP 181	Matches 267; Conservative 19; Mismatches 24; Indels 0; Gaps 0;
Db 121 DRKEIDEVIEELTVKPKVTPICRUPKAQVPGMATHQCESEGHRRPHYSWYRNIDLP 180	Query Match 86.7%; Score 1417; DB 11; Length 310;
Qy 182 TDSRANPRFNSSHLNSETGTLYFTAVHDGSQYCCIASNDAGSARCEBEMEVYDLN 241	Best Local Similarity 86.1%; Score 1417; DB 11; Length 310;
Db 181 TDSRANPRFNSSHLNSETGTLYFTAVHDGSQYCCIASNDAGSARCEBEMEVYDLN 240	1 MALRPPRILCARLPDFELLFRGCLIGAVNLKSSNRTPVQEFSVELSITIDSQTS 60
Qy 242 IGGIIGGVLLVLAVALITLTGICCAVTRGYFINNKDGESTYNPGKPDGVNYIRTDBEGD 301	1 SDPRLEMKIQDQTTYYFDNKIQDGLAIGELGKTSLKINVNTRDSALYRCVARN 120
Db 241 IGGIIGGVLLVLAVALITLTGICCAVTRGYFINNKDGESTYNPGKPDGVNYIRTDBEGD 300	2 SDPRLEMKIQDQTTYYFDNKIQDGLAIGELGKTSLKINVNTRDSALYRCVARN 120
Qy 302 FRHKSSFPVI 310	3 QY 1 NDREKIDEVIEELTVKPKVTPICRUPKAQVPGMATHQCESEGHRRPHYSWYRNIDLP 180
Db 301 FRHKSSFPVI 309	4 Db 1 NDREKIDEVIEELTVKPKVTPICRUPKAQVPGMATHQCESEGHRRPHYSWYRNIDLP 180
Qy 301 FRHKSSFPVI 310	5 Db 1 NDREKIDEVIEELTVKPKVTPICRUPKAQVPGMATHQCESEGHRRPHYSWYRNIDLP 180
Db 301 FRHKSSFPVI 310	6 Qy 1 SDPRLEMKIQDQTTYYFDNKIQDGLAIGELGKTSLKINVNTRDSALYRCVARN 120
Qy 9D8B7 PRELIMINARY; PRT; 310 AA.	7 Db 1 SDPRLEMKIQDQTTYYFDNKIQDGLAIGELGKTSLKINVNTRDSALYRCVARN 120
AC 9D8B7; ID 9D8B7; DT 01-JUN-2001 (TREMBLrel. 17, Created)	8 Qy 1 SDPRLEMKIQDQTTYYFDNKIQDGLAIGELGKTSLKINVNTRDSALYRCVARN 120
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)	9 Db 1 SDPRLEMKIQDQTTYYFDNKIQDGLAIGELGKTSLKINVNTRDSALYRCVARN 120
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)	10 Qy 1 SDPRLEMKIQDQTTYYFDNKIQDGLAIGELGKTSLKINVNTRDSALYRCVARN 120
ID 1110002N23Rik protein	11 Db 1 SDPRLEMKIQDQTTYYFDNKIQDGLAIGELGKTSLKINVNTRDSALYRCVARN 120
GN JCAM3 OR JCAM2 OR 11.0002N23RIK.	12 Qy 1 SDPRLEMKIQDQTTYYFDNKIQDGLAIGELGKTSLKINVNTRDSALYRCVARN 120
Mus musculus (Mouse)	13 Db 1 SDPRLEMKIQDQTTYYFDNKIQDGLAIGELGKTSLKINVNTRDSALYRCVARN 120
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognath; Muridae; Murinae; Mus. NCBI_TaxID=10090; [1]	14 Qy 1 SDPRLEMKIQDQTTYYFDNKIQDGLAIGELGKTSLKINVNTRDSALYRCVARN 120
SEQUENCE FROM N.A. STRAIN=C57BL/6J; TISSUE=Small intestine; MEDLINE=21085660; PubMed=11217851;	15 Db 1 SDPRLEMKIQDQTTYYFDNKIQDGLAIGELGKTSLKINVNTRDSALYRCVARN 120
RX. Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamamoto I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldairelli P., Barich G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hoffman M., Hume D.A., Kamiy M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Monbaerts P., Nordone P., Ring B., Ringold M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seiya T., Shibusawa Y., Suzuki H., Suzuki K., Tohru H., Whittaker C., Wilming L., Wynnshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S., Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection."; EMBL; AK008197; BAB23519.1; -.	16 Qy 1 SDPRLEMKIQDQTTYYFDNKIQDGLAIGELGKTSLKINVNTRDSALYRCVARN 120
RX. Saito R., Okido T., Furuno M., Aono H., Baldairelli P., Barich G., Gustincich S., Hill D., Hoffman M., Hume D.A., Kamiy M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Monbaerts P., Nordone P., Ring B., Ringold M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seiya T., Shibusawa Y., Suzuki H., Suzuki K., Tohru H., Whittaker C., Wilming L., Wynnshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S., Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection."; EMBL; AK008197; BAB23519.1; -.	17 DR PROSTIRE; P550835; IG_LIKE; 2.
MGD; MG1:1933825; Jcam3.	18 DR MGI:1933825; Jcam3.
DR InterPro; IPR003598; Ig-like.	19 DR InterPro; IPR003598; Ig-c2.
DR InterPro; IPR003006; Ig_MHC.	20 DR InterPro; IPR003006; Ig_MHC.
SMART; SM00408; IgC2; 1.	21 SMART; SM00408; IgC2; 1.

RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilmng L., Wynnshaw-Borisi A., Yoshida K., Hasegawa Y., Kawaji H., Kohutsuki S., Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection.", Nature 409:685-690(2001). [3]

RN RP SEQUENCE FROM N.A.

RA STRAUBERG R.; Submitted (MAR-2002) to the EMBL/GenBank/DDJB databases.

RN RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Mesonephros; MEDLINE=22354683; PubMed=12466651;

RA the FANTOM Consortium, the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs", Nature 420:563-573 (2002).

DR EMBL; AK00304; BAC20704.1; -.

DR EMBL; EC024357; AAH24357.1; -.

DR EMBL; AK032833; BAC28049.1; -.

DR MGD; MGI:1933825; Jcam3.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003598; Ig_c2.

DR SMART; SM00408; IgC2_1.

DR PROSITE; PSS0835; Ig_LIKE_2.

KW Immunoglobulin domain.

SQ SEQUENCE 310 AA; 34837 MW; 4B92BCB51D0A4B0A CRC64;

Query Match 86.5%; Score 1415; DB 11; Length 310; Best Local Similarity 86.1%; Pred. No. 3.1e-131; Matches 267; Conservative 18; Mismatches 25; Indels 0; Gaps 0;

Db 1 MAISRRRLRLRLLPDLFLILFRGCLIGAVNLKSSNRTPVVQEFSVELSCIITDSQT 60

Qy 61 SDPRIEWKKIODOQTTVYFFDNKIQDGAIAGRAETLGTSKLWKWNTRDSAYRCEVAR 120

Db 61 SDPRIEWKKIODOQTTVYFFDNKIQDGAIAGRDVFGTSLRKWNTRDSAYRCEVAL 120

Qy 121 NDRKEIDIVELTIVQKPTPVCRYPKAVPGKMATLHQESEGHPHYSWYNDVPL 180

Db 121 NDRKEIDIVELTIVQKPTPVCRYPKAVPGKTAIIQCCQSEGFPHYHSWYNDVPL 180

Qy 181 PTDSRANFRNNSHUNSETGTLVFAVHDQDSGQYVCIASNDASRCBQEMEVYDL 240

Db 181 PTDSRANFRNNSHUNSETGTLVFAVHDQDSGQYVCIASNDASRCBQEMEVYDL 240

Qy 241 NIGGIGGGVVLYLVAVLALITLGTCAYRGFTNNKODGESYTKNPCKPDKGNYIRTEEG 300

Db 241 NIGGIGGGVVLYLVAVLALITLGTCAYRGFTNNKODGESYTKNPCKPDKGNYIRTEEG 300

Qy 301 DFRHKSSFVI 310

Db 301 DFRHKSSFVI 310

RESULTS 6

Q9D1M9 PRELIMINARY; PRT; 310 AA.

AC Q9D1M9; PRELIMINARY; PRT; 310 AA.

DT 01-JUN-2001 (TrEMBLrel. 17, Created)

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE 1110002N23ik protein.

GN JCAM3 OR JCAM2 OR 11_0002N23RIK.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Muridae; Murinae; Mus. OC NCBITaxID=10990; RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Embryo; MEDLINE=21085660; PubMed=11217851;

RA Kawai J., Shinagawa A., Shibutani Y., Konno H., Adachi J., Fukuda S., Arakawa K., Hara A., Fujisawa H., Kondo S., Yamamoto I., Saito T., Okazaki Y., Gejohori T., Bono H., Kasukawa T., Seito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Giessi C., King B., Kochiwa H., Kuehn P., Lewis M., Matsuo I., Pebole G., Quackenbush J., Schirrmann L.M., Staubli F., Suzuki R., Tonita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fleicher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Monbaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schönenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection.", Nature 405:685-690(2001).

DR EMBL; AK003326; BAB22715.1; -.

DR MGD; MGI:1933820; Jcam3.

DR MGD; MGI:1933825; Jcam3.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003598; Ig_C2.

DR InterPro; IPR003006; Ig_MHC.

DR Pfam; PF00047; ig_2.

DR SMART; SM00408; IgC2_1.

DR PROSITE; PS50385; Ig_LIKE_2.

KW Immunoglobulin domain.

SQ SEQUENCE 310 AA; 34819 MW; 6692BCAD68EA4B1D CRC64;

Query Match 85.8%; Score 1403; DB 11; Length 310; Best Local Similarity 85.2%; Pred. No. 4.7e-130; Matches 26; Mismatches 26; Indels 0; Gaps 0;

Db 1 MALRPPRPLCARLPDFELLFLFRGCLIGAVNLKSSNRTPVVQEFSVELSCIITDSQT 60

Qy 1 MALSRRLRLRLLYARLPDFELLFLFRGCLIGAVNLKSSNRTPVVQEFSVELSCIITDSQT 60

Db 1 SDPRLEWKKIODOQTTVYFFDNKIQDGAIAGRAETLGTSKLWKWNTRDSAYRCEVAR 120

Qy 61 SDPRLEWKKIODOQTTVYFFDNKIQDGAIAGRDVFGTSLRKWNTRDSAYRCEVAL 120

Db 61 SDPRLEWKKIODOQTTVYFFDNKIQDGAIAGRDVFGTSLRKWNTRDSAYRCEVAL 120

Qy 121 NDRKEIDIVELTIVQKPTPVCRYPKAVPGKMATLHQESEGHPHYSWYNDVPL 180

Db 121 NDRKEIDIVELTIVQKPTPVCRYPKAVPGKTAIIQCCQSEGFPHYHSWYNDVPL 180

Qy 181 PTDSRANFRNNSHUNSETGTLVFAVHDQDSGQYVCIASNDASRCBQEMEVYDL 240

Db 181 PTDSRANFRNNSHUNSETGTLVFAVHDQDSGQYVCIASNDASRCBQEMEVYDL 240

Qy 241 NIGGIGGGVVLYLVAVLALITLGTCAYRGFTNNKODGESYTKNPCKPDKGNYIRTEEG 300

Db 241 NIGGIGGGVVLYLVAVLALITLGTCAYRGFTNNKODGESYTKNPCKPDKGNYIRTEEG 300

Qy 301 DFRHKSSFVI 310

Db 301 DFRHKSSFVI 310

RESULTS 7

Q9J159 PRELIMINARY; PRT; 298 AA.

AC Q9J159; PRELIMINARY; PRT; 298 AA.

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT	01-OCT-2000 (TREMBLrel. 15; Last sequence update)	Qy	124 -KEIDBIVELTVQVKPVTCPVCRYKAVPVGKMATLHQSEGHPRPHYSWYRNDVPLPT 182
DT	01-MAR-2003 (TREMBLrel. 23; Last annotation update)	Db	119 GQNLDKVNMLEVLVAPAVACEYTSVMTGSUVLRCQDKEGNAPBTWFKDQG----T 174
DB	Vascular endothelial junction-associated molecule (junctional adhesion molecule-3) (241003G21RIK protein).	Qy	183 DSRAPIR--FRNSSHLNSETGTLPVFTAVHKDGGQYCYIASNDAGSARCEEQMEVYD 239
GN	JCAM2 OR JAM-3 OR 241003G21RIK.	Db	175 SLLGPKGKGGTHNNSSYMTNTKSGLIQFNMISKMDGEYICEAARNVGHRCPGRMQLQDV 234
OS	Mus musculus (Mouse)	Qy	240 LNIGGIGGYLVLAVALITLGICCAVRRGYFINNKQDGESYKPGKPGVNYRTDDE 299
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Db	235 LNISGIAVVVVARVISVGLGTCYAQRGYF----SKETSFQKGSP--ASKVTTMSE 287
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI Taxid:10096;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=C57BL/6J;		
RX	Medline=20317114; PubMed=10779521;	Qy	300 GDFRKSSFV 310
RA	Palmer D., van Zante A., Huang C.-C., Hemmerich S., Rosen S.D.; "Vascular Endothelial Junction-associated Molecule, a Novel Member of the Immunoglobulin Superfamily, Is Localized to Intercellular Boundaries of Endothelial Cells.";	Db	288 NDKFRTKSFII 298
RT	"Cloning of JAM-2 and JAM-3: an Emerging Junctional Adhesion Family?";		
RT	Curr. Top. Microbiol. Immunol. 251:91-98(2000).		
RL	J. Biol. Chem. 275:19139-19145(2000).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RX	PubMed=11036763;	Qy	300 GDFRKSSFV 310
RA	Aurrand-Lions M.A., Duncan L., Du Pasquier L., Imhof B.A.; "Cloning of JAM-2 and JAM-3: an Emerging Junctional Adhesion Family?";	Db	288 NDKFRTKSFII 298
RT	Curr. Top. Microbiol. Immunol. 251:91-98(2000).		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=C57BL/6J; TISSUE=Embryo, and Embryonic stem cells; MEDLINE=21085660; PubMed=11217851;	Qy	300 GDFRKSSFV 310
RX	Kawai J., Shinagawa A., Shibusawa K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamamoto R., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Giassi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Paisole G., Quackenbush J., Schriml L.M., Straubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai T., Okido T., Furuno M., Aono R., Baldarelli R., Barsh G., Blake J., Boffelli D., Botunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hoffmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzairelli J., Monbaertis P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seiya T., Shibaoka Y., Storch K.-F., Suzuki H., Toyooka K., Wang K.H., Weitz C., Wittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S., Hayashizaki Y.;	Db	2 ARSPQGLMLLHLTIVALDYHKANGFSASQDKHPEVTLTSDP 63
RA	"Functional annotation of a full-length mouse cDNA collection.";	Qy	300 GDFRKSSFV 310
RL	Nature 409:685-690(2001).	Db	2 ARSPQGLMLLHLTIVALDYHKANGFSASQDKHPEVTLTSDP 63
DR	EMBL: AF255911; AAF81224.1; EMBL: AJ291757; AAC20699.1; EMBL: AK013914; BAB28053.1; EMBL: AK01616; BAB27064.1; MGD: MGI:1933825; Jcam3. DR: MGI:1933825; Jcam3. DR: InterPro: IPRO0110; Ig-like. DR: InterPro: IPRO0306; Ig_MHC. DR: Pfam: PF00047; Ig_2. DR: PROSITE: PS50833; Ig_LIKE. DR: SEQUENCE: 298 AA; 33047 MW; 1124E0F07B6CF751 CRC64;	Qy	300 GDFRKSSFV 310
RT	Best Local Similarity 36.7%; Pred. No. 4.7e-39; Mismatches 53; Conservative 53; Gaps 9;	Db	235 LNISGIAVVVVARVISVGLGTCYAQRGYF----SKETSFQKGSP--ASKVTTMSE 287
SQ	13 ARLPDFFLLFLRGCLIGAVNLKSSN-----RTPVVOFESVELSCITDSQTSDP 63	Qy	300 GDFRKSSFV 310
DR	2 ARSPQGLMLLHLTIVALDYHKANGFSASQDKHPEVTLTSDP 63	Db	288 NDKFRTKSFII 298
RA	64 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Qy	300 GDFRKSSFV 310
RA	61 RLEWKKV-GQGVSLVYYQQQLQGDIDKDRAMEI-DFNIRIKNVTRDAGEYRCEVASAPTEQ 118	Db	235 LNISGIAVVVVARVISVGLGTCYAQRGYF----SKETSFQKGSP--ASKVTTMSE 287
RA	60 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Qy	300 GDFRKSSFV 310
RA	61 RLEWKKV-GQGVSLVYYQQQLQGDIDKDRAMEI-DFNIRIKNVTRDAGEYRCEVASAPTEQ 118	Db	235 LNISGIAVVVVARVISVGLGTCYAQRGYF----SKETSFQKGSP--ASKVTTMSE 287
RA	62 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Qy	300 GDFRKSSFV 310
RA	63 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Db	235 LNISGIAVVVVARVISVGLGTCYAQRGYF----SKETSFQKGSP--ASKVTTMSE 287
RA	64 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Qy	300 GDFRKSSFV 310
RA	65 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Db	235 LNISGIAVVVVARVISVGLGTCYAQRGYF----SKETSFQKGSP--ASKVTTMSE 287
RA	66 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Qy	300 GDFRKSSFV 310
RA	67 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Db	235 LNISGIAVVVVARVISVGLGTCYAQRGYF----SKETSFQKGSP--ASKVTTMSE 287
RA	68 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Qy	300 GDFRKSSFV 310
RA	69 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Db	235 LNISGIAVVVVARVISVGLGTCYAQRGYF----SKETSFQKGSP--ASKVTTMSE 287
RA	70 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Qy	300 GDFRKSSFV 310
RA	71 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Db	235 LNISGIAVVVVARVISVGLGTCYAQRGYF----SKETSFQKGSP--ASKVTTMSE 287
RA	72 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Qy	300 GDFRKSSFV 310
RA	73 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Db	235 LNISGIAVVVVARVISVGLGTCYAQRGYF----SKETSFQKGSP--ASKVTTMSE 287
RA	74 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Qy	300 GDFRKSSFV 310
RA	75 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Db	235 LNISGIAVVVVARVISVGLGTCYAQRGYF----SKETSFQKGSP--ASKVTTMSE 287
RA	76 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Qy	300 GDFRKSSFV 310
RA	77 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Db	235 LNISGIAVVVVARVISVGLGTCYAQRGYF----SKETSFQKGSP--ASKVTTMSE 287
RA	78 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Qy	300 GDFRKSSFV 310
RA	79 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Db	235 LNISGIAVVVVARVISVGLGTCYAQRGYF----SKETSFQKGSP--ASKVTTMSE 287
RA	80 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Qy	300 GDFRKSSFV 310
RA	81 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Db	235 LNISGIAVVVVARVISVGLGTCYAQRGYF----SKETSFQKGSP--ASKVTTMSE 287
RA	82 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Qy	300 GDFRKSSFV 310
RA	83 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Db	235 LNISGIAVVVVARVISVGLGTCYAQRGYF----SKETSFQKGSP--ASKVTTMSE 287
RA	84 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Qy	300 GDFRKSSFV 310
RA	85 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Db	235 LNISGIAVVVVARVISVGLGTCYAQRGYF----SKETSFQKGSP--ASKVTTMSE 287
RA	86 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Qy	300 GDFRKSSFV 310
RA	87 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Db	235 LNISGIAVVVVARVISVGLGTCYAQRGYF----SKETSFQKGSP--ASKVTTMSE 287
RA	88 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Qy	300 GDFRKSSFV 310
RA	89 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Db	235 LNISGIAVVVVARVISVGLGTCYAQRGYF----SKETSFQKGSP--ASKVTTMSE 287
RA	90 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Qy	300 GDFRKSSFV 310
RA	91 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Db	235 LNISGIAVVVVARVISVGLGTCYAQRGYF----SKETSFQKGSP--ASKVTTMSE 287
RA	92 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Qy	300 GDFRKSSFV 310
RA	93 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Db	235 LNISGIAVVVVARVISVGLGTCYAQRGYF----SKETSFQKGSP--ASKVTTMSE 287
RA	94 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Qy	300 GDFRKSSFV 310
RA	95 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Db	235 LNISGIAVVVVARVISVGLGTCYAQRGYF----SKETSFQKGSP--ASKVTTMSE 287
RA	96 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Qy	300 GDFRKSSFV 310
RA	97 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Db	235 LNISGIAVVVVARVISVGLGTCYAQRGYF----SKETSFQKGSP--ASKVTTMSE 287
RA	98 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Qy	300 GDFRKSSFV 310
RA	99 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Db	235 LNISGIAVVVVARVISVGLGTCYAQRGYF----SKETSFQKGSP--ASKVTTMSE 287
RA	100 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Qy	300 GDFRKSSFV 310
RA	101 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Db	235 LNISGIAVVVVARVISVGLGTCYAQRGYF----SKETSFQKGSP--ASKVTTMSE 287
RA	102 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Qy	300 GDFRKSSFV 310
RA	103 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Db	235 LNISGIAVVVVARVISVGLGTCYAQRGYF----SKETSFQKGSP--ASKVTTMSE 287
RA	104 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Qy	300 GDFRKSSFV 310
RA	105 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Db	235 LNISGIAVVVVARVISVGLGTCYAQRGYF----SKETSFQKGSP--ASKVTTMSE 287
RA	106 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Qy	300 GDFRKSSFV 310
RA	107 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Db	235 LNISGIAVVVVARVISVGLGTCYAQRGYF----SKETSFQKGSP--ASKVTTMSE 287
RA	108 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Qy	300 GDFRKSSFV 310
RA	109 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Db	235 LNISGIAVVVVARVISVGLGTCYAQRGYF----SKETSFQKGSP--ASKVTTMSE 287
RA	110 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Qy	300 GDFRKSSFV 310
RA	111 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Db	235 LNISGIAVVVVARVISVGLGTCYAQRGYF----SKETSFQKGSP--ASKVTTMSE 287
RA	112 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Qy	300 GDFRKSSFV 310
RA	113 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Db	235 LNISGIAVVVVARVISVGLGTCYAQRGYF----SKETSFQKGSP--ASKVTTMSE 287
RA	114 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Qy	300 GDFRKSSFV 310
RA	115 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Db	235 LNISGIAVVVVARVISVGLGTCYAQRGYF----SKETSFQKGSP--ASKVTTMSE 287
RA	116 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Qy	300 GDFRKSSFV 310
RA	117 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Db	235 LNISGIAVVVVARVISVGLGTCYAQRGYF----SKETSFQKGSP--ASKVTTMSE 287
RA	118 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Qy	300 GDFRKSSFV 310
RA	119 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Db	235 LNISGIAVVVVARVISVGLGTCYAQRGYF----SKETSFQKGSP--ASKVTTMSE 287
RA	120 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Qy	300 GDFRKSSFV 310
RA	121 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Db	235 LNISGIAVVVVARVISVGLGTCYAQRGYF----SKETSFQKGSP--ASKVTTMSE 287
RA	122 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Qy	300 GDFRKSSFV 310
RA	123 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Db	235 LNISGIAVVVVARVISVGLGTCYAQRGYF----SKETSFQKGSP--ASKVTTMSE 287
RA	124 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Qy	300 GDFRKSSFV 310
RA	125 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Db	235 LNISGIAVVVVARVISVGLGTCYAQRGYF----SKETSFQKGSP--ASKVTTMSE 287
RA	126 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Qy	300 GDFRKSSFV 310
RA	127 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Db	235 LNISGIAVVVVARVISVGLGTCYAQRGYF----SKETSFQKGSP--ASKVTTMSE 287
RA	128 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Qy	300 GDFRKSSFV 310
RA	129 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Db	235 LNISGIAVVVVARVISVGLGTCYAQRGYF----SKETSFQKGSP--ASKVTTMSE 287
RA	130 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Qy	300 GDFRKSSFV 310
RA	131 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Db	235 LNISGIAVVVVARVISVGLGTCYAQRGYF----SKETSFQKGSP--ASKVTTMSE 287
RA	132 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Qy	300 GDFRKSSFV 310
RA	133 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Db	235 LNISGIAVVVVARVISVGLGTCYAQRGYF----SKETSFQKGSP--ASKVTTMSE 287
RA	134 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Qy	300 GDFRKSSFV 310
RA	135 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Db	235 LNISGIAVVVVARVISVGLGTCYAQRGYF----SKETSFQKGSP--ASKVTTMSE 287
RA	136 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Qy	300 GDFRKSSFV 310
RA	137 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Db	235 LNISGIAVVVVARVISVGLGTCYAQRGYF----SKETSFQKGSP--ASKVTTMSE 287
RA	138 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Qy	300 GDFRKSSFV 310
RA	139 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Db	235 LNISGIAVVVVARVISVGLGTCYAQRGYF----SKETSFQKGSP--ASKVTTMSE 287
RA	140 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Qy	300 GDFRKSSFV 310
RA	141 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Db	235 LNISGIAVVVVARVISVGLGTCYAQRGYF----SKETSFQKGSP--ASKVTTMSE 287
RA	142 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Qy	300 GDFRKSSFV 310
RA	143 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Db	235 LNISGIAVVVVARVISVGLGTCYAQRGYF----SKETSFQKGSP--ASKVTTMSE 287
RA	144 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Qy	300 GDFRKSSFV 310
RA	145 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Db	235 LNISGIAVVVVARVISVGLGTCYAQRGYF----SKETSFQKGSP--ASKVTTMSE 287
RA	146 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Qy	300 GDFRKSSFV 310
RA	147 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Db	235 LNISGIAVVVVARVISVGLGTCYAQRGYF----SKETSFQKGSP--ASKVTTMSE 287
RA	148 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Qy	300 GDFRKSSFV 310
RA	149 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Db	235 LNISGIAVVVVARVISVGLGTCYAQRGYF----SKETSFQKGSP--ASKVTTMSE 287
RA	150 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Qy	300 GDFRKSSFV 310
RA	151 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Db	235 LNISGIAVVVVARVISVGLGTCYAQRGYF----SKETSFQKGSP--ASKVTTMSE 287
RA	152 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123	Qy	300 GDFRKSSFV 310
RA	153 RIEWKKIQDQETTYFFDNKIQGDLAGRABLGTSLKIMVNTRDSALXRVCEVARNDR 123</		

Qy	Db	Sequence	Result ID	Score	Length	PRT;	PRIMINARY;	PRT;	AA.	
75	TTCVFPDKIQGDLAGRAELIGKTSUKIWNVTRDSALYCEVVARNDKEIDEIVELT	134	Q9JXDS							
69	TALVCYNSQTATPASYADR-TFSSSGTTESSUTRKNGEYTC-MYSEEGGNNGEYVSIHLT	126	Q9JXDS							
135	VQVKPVTPCVRPKAVPVGKMATLHQESEGHPRPHYSWYRNDVPLPT-DSRANPRFRN	193	Q9JXDS							
Qy	127	VLVPSSKPTISPVSSYTGRAVLTSEHDGSPSEWFKDGSMLTADAKTRAFMS	186	DT	01-OCT-2000	(TREMBLrel.	15;	Created)		
Db	194	SSSHINSETGTIUVFTAVHKDDSGQXYCTIASNDAGSA-RCEQEMEYDYLNIIGGIIGGVLYV	252	DT	01-OCT-2000	(TREMBLrel.	15;	Last sequence update)		
Qy	187	SFTIDPSKGDIIDPVTAFSDGEYQCAQNGYGTAMSRSAHMDADEVLYVIAVLYT	246	DT	01-MAR-2003	(TREMBLrel.	23;	Junctional adhesion molecule (Fragment).		
Db	253	LAVLALITLGICCAVRRGYFVINNKQDGESYKKNPGKDGVNYIRTDDEGGPRHKSSFVI	310	OS	Rat	Rattus norvegicus (Rat).				
Qy	247	LILIGLILIGWWEAATRGYFERTKG---TAPGKXVIVSQSTRSEGPFKQTSSFLV	300	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. [1]_TaxID=10116;					
RESULT 12										
Qy	Q9YFB2	PRELIMINARY;	Q9YFB2	259	AA.					
AC	Q9YFB2;		Q9YFB2;	12,	Created)					
DT	01-NOV-1999	(TREMBLrel.	12;	Last sequence update)						
DT	01-MAR-2003	(TREMBLrel.	12;	Last annotation update)						
OS	Junction adhesion molecule.									
OS	Homo sapiens (Human); Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. [1]_TaxID=9606;									
RN	SEQUENCE FROM N.A.									
LIU Y., NUSRAT A., SCHNELL F.J., WALSH S., REAVES T.A., POCHET M., FROEY C., PARROS C.A.;										
RA	"Human junctional adhesion molecule is expressed by polarized columnar epithelia and regulates tight junction resealing,"									
RA	Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.									
RA	EMBL; AF154005; AA043794; 1.;									
DR	InterPro; IPR007110; 19-like.									
DR	InterPro; IPR003098; 19_c2.									
DR	InterPro; IPR003006; 19_2.									
PFAM; PF00047; 19_2.										
DR	SMART; SM00408; IgG2; 1.									
DR	PROSITE; PS50835; Ig_LIKE; 1.									
KW	Immunoglobulin domain.									
SEQUENCE	259 AA;	28122 MW;	FE38521A9115822D0	CRC64;						
RESULT 14										
Qy	Q8BT59	PRELIMINARY;	Q8BT59							
AC	Q8BT59;		Q8BT59;							
DT	01-MAR-2003	(TREMBLrel.	23;	Created)						
DT	01-MAR-2003	(TREMBLrel.	23;	Last sequence update)						
DT	01-MAR-2003	(TREMBLrel.	23;	Last annotation update)						
OS	Junction cell adhesion molecule 3 (Fragment).									
OS	Mus musculus (Mouse).									
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. [1]_TaxID=10990;									
RN	SEQUENCE FROM N.A.									
RA	The FANTOM Consortium, MEDLINE=C57BL/6J; PUBMED=12466851;									
RA	RA the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of full-length cDNAs."									
RT	Nature 420:563-573 (2002); DR: AK017692; BAC2552; 1.;									
RT	FT NON_TER 1									
SQ	SEQUENCE 64 AA;	6996 MW;	AF46BC30AA6D0C11	CRC64;						
Query Match	20.2%	Score 331;	DB 4;	Length 259;						
Best Local Similarity	29.6%	Pred. No. 2.9e-24;								
Matches	81;	Conservative	44;	Mismatches 111;	Indels 38;	Gaps 7;				
Qy	42	VVQEFEPSVELSCLITDSQTSDPRIWKKIODEQTYVFDFNQKQDLAGRAELGKTSLK	101	102	IWNTTRDSDLALYCEVVARNDKEIDEIVELTYQVKPVPVCRPKAVPVGKMATLHCQ	161				
Db	19	ILPENNPKUSCAY--SGFSSPR--AASYEDRVTFL-----PTGIT 55		56	FKSIVTREDCTYTC-MVFEEGGNSYGEVKVRLIVLVPSPKTPVNIPSSATIGNRAVLTCS	114				
Qy	102	IWNTTRDSDLALYCEVVARNDKEIDEIVELTYQVKPVPVCRPKAVPVGKMATLHCQ	161	115	EQDGSPSPEWTWFKDGVWTFNPKSTRAFNSNSVYLNPTGELVFDPLSASDTEGYSCER	174				
Db	56	ESEGHPRPHYSWYRNDVPLPTDSRANPRFRNSSLHNSETGTLYPTAVKHDGQYCYA	221	222	SNDGSSARCREQ-EMEVYDLDNIGGIGLVLVLAFLTLGICCAVRYCFINNKODGE	280				
Qy	115	EQDGSPSPEWTWFKDGVWTFNPKSTRAFNSNSVYLNPTGELVFDPLSASDTEGYSCER	174	175	RNGYGTPMTSNAVRMEAVENVGVIVAAVLVTLILGLVFGWPAISGHFDFTKRGTS	234				
Db	222	SNDGSSARCREQ-EMEVYDLDNIGGIGLVLVLAFLTLGICCAVRYCFINNKODGE	280	281	S----YKNPGKPDGVNYIRTDDEGDFRHKSFSV	310				
Qy	175	RNGYGTPMTSNAVRMEAVENVGVIVAAVLVTLILGLVFGWPAISGHFDFTKRGTS	234	235	SKKVYSQPS-----ARSEGFEFKQTSFLV	259				
Db	281	S----YKNPGKPDGVNYIRTDDEGDFRHKSFSV	310	235	SKKVYSQPS-----ARSEGFEFKQTSFLV	259				

Qy 247 GGVLVYLAVLALITLGICCAVRGGYFINKQDGESYKNPGKPDGYNYIRTDEEGDFRHK\$ 306
 Db 1 GGVLVYLAVLTMGICCAVRGGCFSKQDGESTSPGRHDGYNYIRTSEEGFRHK\$ 60

Qy 307 SFVI 310
 Db 61 SFVI 64

RESULT 15

Q91664	PRELIMINARY;	PRT;	318 AA.
ID			
AC	Q91664;		
DT	01-NOV-1996 (TREMBLrel. 01; Created)		
DT	01-NOV-1996 (TREMBLrel. 01; Last sequence update)		
DT	01-MAR-2003 (TREMBLrel. 23; Last annotation update)		
DB			
OS	Xenopus laevis (African clawed frog).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;		
OC	Xenopodinae; Xenopus.		
OX	NCBI_TAXID=8355;		
RN			
RP	SEQUENCE FROM N.A.		
RC	STRAIN=ff; TISSUE=Thymus;		
RX	MEDLINE=96210130; PubMed=8625968;		
RA	Chretien I., Robert J., Marcuz A., Garcia-Sanz J.A., Courtet M., Du Pasquier L.		
RT	"CTX, a novel molecule specifically expressed on the surface of cortical thymocytes in Xenopus".		
RL	Eur. J. Immunol. 26:780-791(1996).		
DR	EMBL; U43340; AAC59899.1; -.		
DR	InterPro: IPR003599; Ig.		
DR	InterPro: IPR007110; Ig-like.		
DR	InterPro: IPR001006; Ig_MHC.		
PFam	PF00047; Ig; 2.		
SMART	SM00409; Ig; 2.		
PROSITE	PS00835; Ig_LIKE; 2.		
SEQUENCE	318 AA; 34429 MW; 6231D24B0B806C09 CRC64;		

Query Match 15.2%; Score 248; DB 13; Length 318;
 Best Local Similarity 26.0%; Pred. No. 68-16; Matches 70; Conservative 57; Mismatches 92; Indels 50; Gaps 10;

Matches 19 FILLFLRCLIGAVN--LKSSNRTPV--VQEESVELSC--IITDSOTSDPRIEK-- 68

Db 3 FLIFITGLSLTLASHCVQTQNPLINTVSQNLTYCYTILNNQNKKNLVIQNNIQA 62

Qy 69 KIQDEQTYVF -----FDNKIQGDLGRAELIGKTSLIKIVNTRRDSDLALYCEVV 118

Db 63 KSONQETYFFYQNGQSLSPSYKRNRTAAMSP----GNAATITISNMQSQDTGIVTCVEL 117

Qy 119 ARNDRKEYDEIVTELYQVKPVPVCPVRYPKAVPVGKMAHLQEQESECHPRPHYSWYRNDV 178

Db 118 -NLPESSGGOKLILTVLVPSPVPHCSRGAVETGHFISLLCYSEGMPPRIYSNNRVE- 174

Qy 179 PLPTDSRANPFRNSSSHNLSETGTLYTAVERKDDSCQYCLIASNDGASARCEEQMEVY 238

Db 175 -----NGLLKSTPSONMQQKGSLTIGNLTDFFEGYRCTASNLLGNATCE-----L 220

Qy 239 DINIGG-----IIGGVLVVLAIALI 259

Db 221 NHFTGEGEGVIAAVIGLLAAIIIAV 249